

Figure 1
Nucleotide Sequence and predicted protein for HLTDG74

-88	10	30	50	
	GTTTGCTCTGGGCAGCCAAGTTGGCATATTGGAAGCTTTTCCGGGCTCTGGAGGAGGGT-29			
-28	70	90	110	31
-8	CCCTGCTTCTTCCTACAGCCGTTCCGGGCATGGCCTGGCTGGGGGCGTCGCTCCACGTCT			11
	M A W L G A S L H V W			
32	130	150	170	91
12	GGGGTTGGCTAATGCTCGGCAGCTGCCTCCTGGCCAGAGCCCAGCTGGATTCTGATGGCA			31
	G W L M L G S C L L A R A Q L D S D G T			
92	190	210	230	151
32	CCATCACTATAGAGGAGCAGATTGCTCTTGCTGAAAGCGAAAGTACAATGTGAACTCA			51
	I T I E E Q I V L V L K A K V Q C E L N			
152	250	270	290	211
52	ACATCACAGCTCAACTCCAGGAGGGAGAAGGTAATTGTTTCCCTGAATGGGATGGACTCA			71
	I T A Q L Q E G E G N C F P E W D G L I			
212	310	330	350	271
72	TTTGTTGGCCCAGAGGAACAGTGGGGAAAATATCGGCTGTTCCATGCCCTCCTTATATTT			91
	C W P R G T V G K I S A V P C P P Y I Y			
272	370	390	410	331
92	ATGACTTCAACCATAAAGGAGTTGCTTTCCGACACTGTAACCCCAATGGAACATGGGATT			111
	D F N H K G V A F R H C N P N G T W D F			
332	430	450	470	391
112	TTATGCACAGCTTAAATAAAACATGGGCCAATTATTCAGACTGCCTTCGCTTCTGCAGC			131
	M H S L N K T W A N Y S D C L R F L Q P			
392	490	510	530	451
132	CAGATATCAGCATAGGAAAGCAAGAATTCTGTGAACGCCTCTATGTAATGTATACCGTTG			151
	D I - S - I G K Q E F C E R L Y V M Y T V G			
452	550	570	590	511
152	GCTACTCCATCTCTTTTGGTTCCTTGGCTGTGGCTATTCTCATCATTGGTTACTTCAGAC			171
	Y S I S F G S L A V A I L I I G Y F R R			
512	610	630	650	571
172	GATTGCATTGCACTAGGAAGTATATCCACATGCACTTATTGTGTCTTTCATGCTGAGAG			191
	L H C T R N Y I H M H L F V S F M L R A			
572	670	690	710	631
192	CTACAAGCATCTTTGTCAAAGACAGAGTAGTCCATGCTCACATAGGAGTAAAGGAGCTGG			211
	T S I F V K D R V V H A H I G V K E L E			

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FIGURE 1

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632	730	750	770	691
212	AGTCCCTAATAATGCAGGATGACCCACAAAATTCCATTGAGGCAACTTCTGTGGACAAAT			231
	S L I M Q D D P Q N S I E A T S V D K S			
692	790	810	830	751
232	CACAAATATATCGGGTGCAAGATTGCTGTTGTGATGTTTATTTACTTCCTGGCTACAAATT			251
	Q Y I G C K I A V V M F I Y F L A T N Y			
752	850	870	890	811
252	ATTATTGGATCCTGGTGGAAGGTCTCTACCTGCATAATCTCATCTTTGTGGCTTTCTTTT			271
	Y W I L V E G L Y L H N L I F V A F F S			
812	910	930	950	871
272	CGGACACCAAATACCTGTGGGGCTTCATCTTGATAGGCTGGGGGTTTCCAGCAGCATTTG			291
	D T K Y L W G F I L I G W G F P A A F V			
872	970	990	1010	931
292	TTGCAGCATGGGCTGTGGCACGAGCAACTCTGGCTGATGCGAGGTGCTGGGAACCTTAGTG			311
	A A W A V A R A T L A D A R C W E L S A			
932	1030	1050	1070	991
312	CTGGAGACATCAAGTGGATTTATCAAGCACCGATCTTAGCAGCTATTGGGCTGAATTTTA			331
	G D I K W I Y Q A P I L A A I G L N F I			
992	1090	1110	1130	1051
332	TTCTGTTTCTGAATACGGTTAGAGTTCTAGCTACCAAATCTGGGAGACCAATGCAGTTG			351
	L F L N T V R V L A T K I W E T N A V G			
1052	1150	1170	1190	1111
352	GGCATGACACAAGGAAGCAATACAGGAAACTGGCCAAATCGACACTGGTCCTGGTCCTAG			371
	H D T R K Q Y R K L A K S T L V L V L V			
1112	1210	1230	1250	1171
372	TCTTTGGAGTGCATTACATCGTGTTCGTGTGCCTGCCTCACTCCTTCACTGGGCTCGGGT			391
	F G V H Y I V F V C L P H S F T G L G W			
1172	1270	1290	1310	1231
392	GGGAGATCCGCATGCACTGTGAGCTCTTCTTCAACTCCTTTCAGGGTTTCTTTGTGTCTA			411
	E I R M H C E L F F N S F Q G F F V S I			
1232	1330	1350	1370	1291
412	TCATCTACTGCTACTGCAATGGAGAGGTTTCAGGCAGAGGTGAAGAAGATGTGGAGTCGGT			431
	I Y C Y C N G E V Q A E V K K M W S R W			
1292	1390	1410	1430	1351
432	GGAATCTCTCCGTGGACTGGAAAAGGACACCGCCATGTGGCAGCCGAGATGCGGCTCAG			451
	N L S V D W K R T P P C G S R R C G S V			
1352	1450	1470	1490	1411
452	TGCTCACCACCGTGACGCACAGCACCAGCAGCCAGTCACAGGTGGCGGCAGCACACGCAT			471
	L T T V T H S T S S Q S Q V A A A H A W			
	1510	1530	1550	

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FIGURE

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1412 GGTGCTTATCTCTGGCAAAGCTGCCAAGATCGCCAGCAGACAGCCTGACAGCCACATCAC 1471
472 C L S L A K L P R S P A D S L T A T S L 491

1570 1590 1610
1472 TTACCTGGCTATGTCTGGAGTAACTCAGAGCAGGACTGCCTCACACACTCTCTCCACGA 1531
492 Y L A M S G V T Q S R T A S H T L S T R 511

1630 1650 1670
1532 GGAGCAACAAGGAAGATAGTGGGAGGCAGAGAGATGATATTCTAATGGAGAAGCCTTCCA 1591
512 S N K E D S G R Q R D D I L M E K P S R 531

1690 1710 1730
1592 GGCCTATGGAATCTAACCCAGACACTGAAGGATGACAAGGAGAACTGAGGATGTTCTCT 1651
532 P M E S N P D T E G 541

1750 1770 1790
1652 GAATGGACATGTGTGGCTGACTTTTCATGGGCTGGTCCAATGGCTGGTTGTGTGAGAGGGC 1711

1810 1830 1850
1712 TTGGCTGATACTCCTATGCTTGAGCACAAAGGCTGAAAATTCAGTTAAGGTGTTACTTAA 1771

1870 1890 1910
1772 TAATAGTTTTTAGGCTCCATGAATTGGCTCCTGTAAATACTAACGACATGAAAATGCAAG 1831

1930 1950 1970
1832 TGTCAATGGAGTAGTTTATTACCTTCTATTGGCATCAAGTTTTCTCTAAATTAATGTAT 1891

1990
1892 GGTATTTGCTCTGTGATTGTTCA 1914

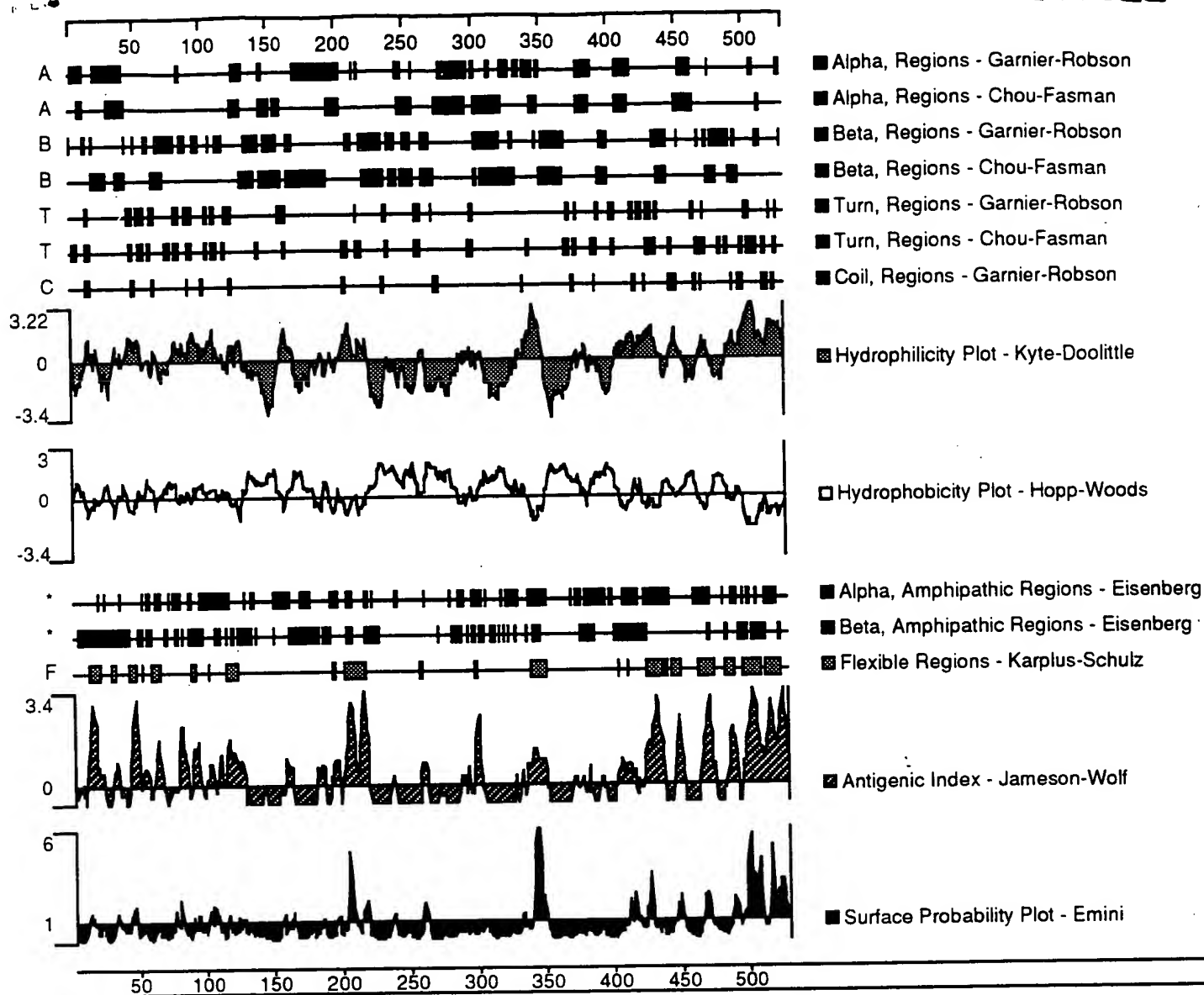
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FIGURE 1 3/3

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FIGURE 2 1/1

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Sequences producing High-scoring Segment Pairs:

Reading ~~Frame~~ Probability
Frame Score P(N)

08^N 468011

gp M74445 OPOPTHYR_1	parathyroid hormone receptor [Di...	+3	597	8.2e-204	6
pir S A39286	parathyroid hormone / parathyroi...	+3	597	2.9e-203	6
gp L04308 HUMPTHYR_1	parathyroid hormone receptor [Ho...	+3	580	6.7e-190	5
pir S S29610	parathyroid hormone receptor - h...	+3	580	6.1e-189	5
gp M77184 RATPATHYR_1	parathyroid hormone receptor [Ra...	+3	576	7.7e-188	5
gp X78936 MMPHRPR_1	parathyroid hormone/parathyroid ...	+3	576	7.7e-188	5
pir S A42698	parathyroid hormone and parathyr...	+3	576	7.7e-188	5
gp L34611 MUSPTHYR06_1	parathyroid hormone/parathyroid ...	+3	576	4.1e-174	5
gp U11087 HSV1RG9_1	vasoactive intestinal peptide 1 ...	+3	319	1.2e-98	5
gp M86835 RATVASREC_1	vasoactive intestinal polypeptid...	+3	254	3.1e-91	5

WARNING: Descriptions of 49 database sequences were not reported due to the limiting value of parameter V = 10.

>gp|M74445|OPOPTHYR_1 parathyroid hormone receptor [Didelphis virginiana]
Length = 585

Plus Strand HSPs:

Score = 597 (274.6 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204
Identities = 108/172 (62%), Positives = 136/172 (79%), Frame = +3

Query: 729 IMQDDPQNSIEATSVDKSQYIGCKIAVVMFIYFLATNYYWILVEGLYLHNLIFVAFFSDT 908
I +++ + E DK+ ++GC++AV +F+YFL TNYWILVEGLYLH+LIF+AFFS+
Sbjct: 253 ITEEELRAFTEPPPADKAGFVGCRVAVTVFLYFLTTNYYWILVEGLYLHSLIFMAFFSEK 312

Query: 909 KYLWGFILIGWGFPAAFVAWAVARATLADARCWELSAGDIKWIYQAPILAAIGLNFIIF 1088
KYLWGF L GWG PA FVA W RATLA+ CW+LS+G+ KWI Q PILAAI +NFIIF
Sbjct: 313 KYLWGFITLFGWGLPAVFVAVWVTVRATLANTECWDLSSGNKKWIIQVPILAAIVVNFIF 372

Query: 1089 LNTVRVLATKIWETNAVGHDTQRKRLAKSTLVVLVLFVGVHYIVFVCLPHS 1244
+N +RVLATK+ ETNA DTR+QYRKL KSTLVL+ +FGVHYIVF+ P++
Sbjct: 373 INIIRVLATKLRETNAGRCDTROQYRKLKSTLVLMPLFGVHYIVFMATPYT 424

Score = 284 (130.6 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204
Identities = 42/70 (60%), Positives = 55/70 (78%), Frame = +3

Query: 267 EGNCFPEWDGLICWPRTVGKISAVPCPPYIYDFNHKGVAFRHCNPNGTWDFMHSNLKNTW 446
+G C PEWD ++CWP G GK+ AVPCP YIYDFNHKG A+R C+ NG+W+ + N+TW
Sbjct: 102 DGFCLPEWDNIVCWPAGVPGKVAVPCPDYIYDFNHKGRAVRRCDSSNGSWELVPGNNRTW 161

Query: 447 ANYSDCLRFL 476
ANYS+C++FL
Sbjct: 162 ANYSECVKFL 171

Score = 279 (128.3 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204
Identities = 51/81 (62%), Positives = 67/81 (82%), Frame = +3

Query: 498 KQEFCELYVMYTVGYSSIFGSLAVAILIIGYFRRLHCTRNYIHMHLFVSFMLRATSIFV 677
++E +RL ++YTVGYSSIFGSL VA+LI+GYFRRLHCTRNYIHMHLFVSFMLRA SIF+
Sbjct: 177 EREVFDRLGMIYTVGYSSIFGSLTAVLILGYFRRLHCTRNYIHMHLFVSFMLRAVSIFI 236

Query: 678 KDRVVHAHIGVKELESIMQD 740
KD V+++ + E+E + ++
Sbjct: 237 KDAVLYSGVSTDEIERITEEE 257

Score = 232 (106.7 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204
Identities = 38/59 (64%), Positives = 50/59 (84%), Frame = +3

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Query: 1248 TGLGWEIRMHCELFNSFQGFVSIICYCNGEVQAEVKMWSRWNLSDWKRTPPCGS 1424

FIGURE 3 1/2 325800-458

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+G+ W+++MH E- FQGFFV+IIYC+CNGEVQAE+KK WSRW +KR GS
Sbjct: 427 SGILWQVQMHYEMLFNSFQGGFFVAIIYCFCNGEVQAEIKKSWSRWTLALDFKRKARSGS 485

Score = 72 (33.1 bits), Expect = $8.2e-204$, Sum P(6) = $8.2e-204$
Identities = 16/37 (43%), Positives = 23/37 (62%), Frame = +3

Query: 159 AQLSDSGTITIEEQIVLVLKAKVQCELNITAQLQEGE 269
A +D+D IT EEQI+L+ A+ QCE + L+ E
Sbjct: 24 ALVDADDVITKEEQIILLRNAQAQCEQRLKEVLRVPE 60

Score = 39 (17.9 bits), Expect = $8.2e-204$, Sum P(6) = $8.2e-204$
Identities = 9/23 (39%), Positives = 12/23 (52%), Frame = +2

Query: 1508 ISGKAAKIASRQPD SHITLPGYV 1576
+S + A A + H LPGYV
Sbjct: 512 LSPRLAPGAGASANGHHQLPGYV 534

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FIGURE 3 2/2 325800-458